



TECH

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/443,986C

DATE: 02/04/2003

TIME: 13:14:34

Input Set : A:\EP.txt

Output Set: N:\CRF4\02042003\I443986C.raw

3 <110> APPLICANT: Elan Corporation
 4 O'Mahony, Daniel J.
 6 <120> TITLE OF INVENTION: RETRO-INVERSION PEPTIDES THAT TARGET GIT TRANSPORT RECEPTORS
 AND RELATED
 7 METHODS
 9 <130> FILE REFERENCE: 25,478-A USA
 11 <140> CURRENT APPLICATION NUMBER: US 09/443,986C
 12 <141> CURRENT FILING DATE: 1999-11-19
 14 <160> NUMBER OF SEQ ID NOS: 85
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 15
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Artificial Sequence
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: PAX2 15 mer fragment-D form retroinversion
 26 <400> SEQUENCE: 1
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 29 1 5 10 15
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 16
 34 <212> TYPE: PRT
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: P31 16 mer fragment- D form retroinversion
 40 <400> SEQUENCE: 2
 42 Gly Pro His Arg Arg Gly Arg Pro Asn Ser Arg Ser Ser Lys Arg Thr
 43 1 5 10 15
 46 <210> SEQ ID NO: 3
 47 <211> LENGTH: 14
 48 <212> TYPE: PRT
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: HAX42 14 mer fragment-D form retroinversion
 54 <400> SEQUENCE: 3
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 57 1 5 10
 60 <210> SEQ ID NO: 4
 61 <211> LENGTH: 15
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
 66 <223> OTHER INFORMATION: PAX2 15 mer fragment
 68 <400> SEQUENCE: 4

Rb
ENTERED

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70 Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu Arg Thr Arg
71 1 5 10 15
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 16
76 <212> TYPE: PRT
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: P31 16 mer fragment
82 <400> SEQUENCE: 5
84 Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro Gly
85 1 5 10 15
88 <210> SEQ ID NO: 6
89 <211> LENGTH: 14
90 <212> TYPE: PRT
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: HAX42 14 mer fragment
96 <400> SEQUENCE: 6
98 Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly
99 1 5 10
102 <210> SEQ ID NO: 7
103 <211> LENGTH: 40
104 <212> TYPE: PRT
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: PAX2 full length
110 <400> SEQUENCE: 7
112 Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val Asp
113 1 5 10 15
116 Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg Leu
117 20 25 30
120 Arg Thr Arg Ser Arg Pro Asn Gly
121 35 40
124 <210> SEQ ID NO: 8
125 <211> LENGTH: 45
126 <212> TYPE: PRT
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: HAX42 full length, N-terminal Lysine is dansylated
132 <220> FEATURE:
133 <221> NAME/KEY: MOD_RES
134 <222> LOCATION: (1)..(1)
135 <223> OTHER INFORMATION: Dansylated L-Lysine
138 <400> SEQUENCE: 8
140 Lys Ser Asp His Ala Leu Gly Thr Asn Leu Arg Ser Asp Asn Ala Lys
141 1 5 10 15
144 Glu Pro Gly Asp Tyr Asn Cys Cys Gly Asn Gly Asn Ser Thr Gly Arg
145 20 25 30
148 Lys Val Phe Asn Arg Arg Pro Ser Ala Ile Pro Thr

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Input Set : A:\EP.txt
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149 35 40 45
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 153 <211> LENGTH: 16
 154 <212> TYPE: PRT
 155 <213> ORGANISM: Artificial Sequence
 157 <220> FEATURE:
 158 <223> OTHER INFORMATION: ZElan 144; PAX2 15 mer fragment-D form retroinversion with
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 159 tional L-lysine in position 1
 161 <220> FEATURE:
 162 <221> NAME/KEY: MOD_RES
 163 <222> LOCATION: (1)..(1)
 164 <223> OTHER INFORMATION: Dansylated L-lysine
 167 <400> SEQUENCE: 9
 169 Lys Arg Thr Arg Leu Arg Arg Asn His Ser Ser His Lys Ala Asn Thr
 170 1 5 10 15
 173 <210> SEQ ID NO: 10
 174 <211> LENGTH: 17
 175 <212> TYPE: PRT
 176 <213> ORGANISM: Artificial Sequence
 178 <220> FEATURE:
 179 <223> OTHER INFORMATION: ZElan 145; P31 16 mer fragment- D form retroinversion with
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 180 onal L-lysine in position 1
 182 <220> FEATURE:
 183 <221> NAME/KEY: MOD_RES
 184 <222> LOCATION: (1)..(1)
 185 <223> OTHER INFORMATION: dansylated L-lysine
 188 <400> SEQUENCE: 10
 190 Lys Gly Pro His Arg Arg Gly Arg Pro Asn Ser Arg Ser Ser Lys Arg
 191 1 5 10 15
 194 Thr
 198 <210> SEQ ID NO: 11
 199 <211> LENGTH: 15
 200 <212> TYPE: PRT
 201 <213> ORGANISM: Artificial Sequence
 203 <220> FEATURE:
 204 <223> OTHER INFORMATION: ZElan 146; HAX42 14 mer fragment-D form retroinversion with
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 205 ional L-Lysine in position 1
 207 <220> FEATURE:
 208 <221> NAME/KEY: MOD_RES
 209 <222> LOCATION: (1)..(1)
 210 <223> OTHER INFORMATION: dansylated L-Lysine
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 216 1 5 10 15
 219 <210> SEQ ID NO: 12
 220 <211> LENGTH: 16
 221 <212> TYPE: PRT
 222 <213> ORGANISM: Artificial Sequence
 224 <220> FEATURE:

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Input Set : A:\EP.txt
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225 <223> OTHER INFORMATION: ZElan 129; PAX2 15 mer fragment with additional L-Lysine in
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226 tition 1
228 <220> FEATURE:
229 <221> NAME/KEY: MOD_RES
230 <222> LOCATION: (1)..(1)
231 <223> OTHER INFORMATION: dansylated L-Lysine
234 <400> SEQUENCE: 12
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237 1 5 10 15
240 <210> SEQ ID NO: 13
241 <211> LENGTH: 17
242 <212> TYPE: PRT
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: ZElan 031; P31 16 mer fragment with additional L-Lysine in
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247 on 1
249 <220> FEATURE:
250 <221> NAME/KEY: MOD_RES
251 <222> LOCATION: (1)..(1)
252 <223> OTHER INFORMATION: dansylated L-Lysine
255 <400> SEQUENCE: 13
257 Lys Thr Arg Lys Ser Ser Arg Ser Asn Pro Arg Gly Arg Arg His Pro
258 1 5 10 15
261 Gly
265 <210> SEQ ID NO: 14
266 <211> LENGTH: 15
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: ZElan 091; HAX42 14 mer fragment with additional L-lysine in
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272 tition 1
274 <220> FEATURE:
275 <221> NAME/KEY: MOD_RES
276 <222> LOCATION: (1)..(1)
277 <223> OTHER INFORMATION: dansylated L-lysine
280 <400> SEQUENCE: 14
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283 1 5 10 15
286 <210> SEQ ID NO: 15
287 <211> LENGTH: 41
288 <212> TYPE: PRT
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: PAX2 full length, N-terminal Lysine is dansylated
294 <220> FEATURE:
295 <221> NAME/KEY: MOD_RES
296 <222> LOCATION: (1)..(1)
297 <223> OTHER INFORMATION: dansylated L-Lysine
300 <400> SEQUENCE: 15

RAW SEQUENCE LISTING
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Input Set : A:\EP.txt
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302 Lys Ser Thr Pro Pro Ser Arg Glu Ala Tyr Ser Arg Pro Tyr Ser Val
303 1 5 10 15
306 Asp Ser Asp Ser Asp Thr Asn Ala Lys His Ser Ser His Asn Arg Arg
307 20 25 30
310 Leu Arg Thr Arg Ser Arg Pro Asn Gly
311 35 40
314 <210> SEQ ID NO: 16
315 <211> LENGTH: 44
316 <212> TYPE: PRT
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: S15 44 mer fragment L-form
322 <400> SEQUENCE: 16
324 Arg Ser Gly Ala Tyr Glu Ser Pro Asp Gly Arg Gly Gly Arg Ser Tyr
325 1 5 10 15
328 Val Gly Gly Gly Gly Cys Gly Asn Ile Gly Arg Lys His Asn Leu
329 20 25 30
332 Trp Gly Leu Arg Thr Ala Ser Pro Ala Cys Trp Asp
333 35 40
336 <210> SEQ ID NO: 17
337 <211> LENGTH: 44
338 <212> TYPE: PRT
339 <213> ORGANISM: Artificial Sequence
341 <220> FEATURE:
342 <223> OTHER INFORMATION: S21 44 mer fragment L-form
344 <400> SEQUENCE: 17
346 Ser Pro Arg Ser Phe Trp Pro Val Val Ser Arg His Glu Ser Phe Gly
347 1 5 10 15
350 Ile Ser Asn Tyr Leu Gly Cys Gly Tyr Arg Thr Cys Ile Ser Gly Thr
351 20 25 30
354 Met Thr Lys Ser Ser Pro Ile Tyr Pro Arg His Ser
355 35 40
358 <210> SEQ ID NO: 18
359 <211> LENGTH: 44
360 <212> TYPE: PRT
361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
364 <223> OTHER INFORMATION: S22 44 mer fragment L-form
366 <400> SEQUENCE: 18
368 Ser Ser Ser Ser Asp Trp Gly Gly Val Pro Gly Lys Val Val Arg Glu
369 1 5 10 15
372 Arg Phe Lys Gly Arg Gly Cys Gly Ile Ser Ile Thr Ser Val Leu Thr
373 20 25 30
376 Gly Lys Pro Asn Pro Cys Pro Glu Pro Lys Ala Ala
377 35 40
380 <210> SEQ ID NO: 19
381 <211> LENGTH: 44
382 <212> TYPE: PRT
383 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:73; Xaa Pos. 1,3,4,6,7,8,10
Seq#:74; Xaa Pos. 2,4,7,8
Seq#:75; Xaa Pos. 7,8

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6